

SEQUENCE LISTING

<110> Fisher F., Eric Edwards K., Carl Kieft L., Gary

<120> Truncated Soluble Tumor Necrosis Factor Type-I and Type-II Receptors

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<140> 09/882,735

<141> 2001-06-15

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<151> 1999-01-08

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<150> 60/039,792

<151> 1997-03-04

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Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys
20 25 30

cca ggc c Pro Gly P													144
ttc acc g Phe Thr A 50		_			_		_		_	-			192
tgc cga a Cys Arg L 65			Gln 'Gln										240
cgg gac a Arg Asp T													288
agt gaa a Ser Glu A													336
acc gtg c Thr Val H													384
cat gca g His Ala G 130													432
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Ile Cys C	ys Thr 20	Lys Cy	His	Lys	Gly 25	Thr	Tyr	Leu	Tyr	Asn 30	Asp	Cys	
Pro Gly P	ro Gly 35	Gln As	Thr	Asp 40	Cys	Arg	Glu	Cys	Glu 45	Ser	Gly	Ser	
Phe Thr A	la Ser	Glu Ası	His 55	Leu	Arg	His	Cys	Leu 60	Ser	Cys	Ser	Lys	
Cys Arg L 65	ys Glu	Met Gl		Val	Glu	Ile	Ser 75	Ser	Cys	Thr	Val	Asp 80	

Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly 100 105 110	
Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys 115 120 125	
His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn 130 135 140	
Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu 145 150 155 160	
Asn	
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Asn Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn

2.0	25	3.0

gac tgt cca ggc ccg ggg cag gat acg gac tgc agg gag tgt gag agc 144
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35 40 45

ggc tcc ttc acc gct tca gaa aac cac ctc aga cac tgc ctc agc tgc 192
Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys
50 55 60

tcc aaa tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca 240 Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr 65 70 75

gtg gac cgg gac acc gtg tgt ggc tgc agg aag aac cag tac cgg cat 288
Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His
80 85 90 95

tat tgg agt gaa aac ctt ttc cag tgc ttc aat tgc tct ctg taaaagctt 339
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Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly 35 40 45

Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser 50 55 60

Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val 65 70 75 80

Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr
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gtg gac cgg gac acc gtg tgt ggt tgc agg aag aac cag tac cgg cat 288 Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His 80 85 90 95											
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Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp 20 25 30											

Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly 35 Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser 55 Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val 70 Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn 100 <210> 9 <211> 285 <212> DNA <213> Artificial Sequence <223> Description of Artificial Sequence: sTNFR-I 2.3D/d18<220> <221> CDS <222> (4)..(276) <400> 9 cat atg tgt acc aag tgc cac aaa gga acc tac ttg tac aat gac tgt Met Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys 1.0 cca ggc ccg ggg cag gat acg gac tgc agg gag tgt gag agc ggc tcc 96 Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser 2.0 144 ttc acc qct tca qaa aac cac ctc aga cac tgc ctc agc tgc tcc aaa Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys 40 35 tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca gtg gac 192 Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp 50 240 cgg gac acc gtg tgt ggc tgc agg aag aac cag tac cgg cat tat tgg Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp 65 285 agt gaa aac ctt ttc cag tgc ttc aat tgc tct ctg taaaagctt Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu 80

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Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn H:	is										
Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly G 50 55 60	ln										
Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cy 65 70 75	/s 30										
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aca gtg gac Thr Val Asp 65			Cys									240
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taaaagctt												294
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														tgc Cys		96
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														agc Ser		240
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														ggg Gly		336
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aga Arg	cca Pro 130	gga Gly	act Thr	gaa Glu	aca Thr	tca Ser 135	gac Asp	gtg Val	gtg Val	tgc Cys	aag Lys 140	ccc Pro	tgt Cys	gcc Ala	ccg Pro	432
999 Gly 145														ccc Pro		480
														gat Asp 175		528
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180 185 190

cac tta ccc cag cca gtg tcc aca cga tcc caa cac acg cag cca act
His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr
195

cca gaa ccc agc act gct cca agc acc tcc ttc ctg ctc cca atg ggc
Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly
210

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225

705

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Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu 50 55 60

Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser 65 70 75 80

Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys
85 90 95

Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys
100 105 110

Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala 115 120 125

Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro 130 135 140

Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His 145 150 155 160

Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Arg Asp Ala 165 170 175

Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val 180 185 190

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His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr
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occua;	good thoughgus and games of	
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12137	Michiela bequeñec	
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	01190#11	
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